

#6

SEQUENCE LISTING



<110> MIZUTANI, Masako
TANAKA, Yoshikazu
KUSUMI, Takaaki
SAITO, Kazuki
YAMAZAKI, Mami
ZHIZHONG, Gong

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ACTIVITY

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<140> 09/147,955

<141> 1999-03-24

<150> PCT/JP98/03199

<151> 1998-07-16

<150> JP 9-200571

<151> 1997-07-25

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Ile Asn Pro Ala Leu Gln Phe Ala Lys Arg Leu Ala Asn Ala Asp Ile
20 25 30
Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Trp Arg Arg Met Ser Arg
35 40 45
Thr Ala Ala Gly Ser Asn Gly Leu Ile Asn Phe Val Ser Phe Ser Asp
50 55 60
Gly Tyr Asp Asp Gly Leu Gln Pro Gly Asp Asp Gly Lys Asn Tyr Met
65 70 75 80
Ser Glu Met Lys Ser Arg Gly Ile Lys Ala Leu Ser Asp Thr Leu Ala
85 90 95
Ala Asn Asn Val Asp Gln Lys Ser Ser Lys Ile Thr Phe Val Val Tyr
100 105 110
Ser His Leu Phe Ala Trp Ala Ala Lys Val Ala Arg Glu Phe His Leu
115 120 125
Arg Ser Ala Leu Leu Trp Ile Glu Pro Ala Thr Val Leu Asp Ile Phe
130 135 140
Tyr Phe Tyr Phe Asn Gly Tyr Ser Asp Glu Ile Asp Ala Gly Ser Asp
145 150 155 160
Ala Ile His Leu Pro Gly Gly Leu Pro Val Leu Ala Gln Arg Asp Leu
165 170 175
Pro Ser Phe Leu Leu Pro Ser Thr His Glu Arg Phe Arg Ser Leu Met
180 185 190
Lys Glu Lys Leu Glu Thr Leu Glu Gly Glu Glu Lys Pro Lys Val Leu
195 200 205
Val Asn Ser Phe Asp Ala Leu Glu Pro Asp Ala Leu Lys Ala Ile Asp
210 215 220
Lys Tyr Glu Met Ile Ala Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu
225 230 235 240
Asp Gly Lys Asp Pro Ser Asp Arg Ser Phe Gly Gly Asp Leu Phe Glu
245 250 255
Lys Gly Ser Asn Asp Asp Asp Cys Leu Glu Trp Leu Ser Thr Asn Pro
260 265 270
Arg Ser Ser Val Val Tyr Val Ser Phe Gly Ser Phe Val Asn Thr Thr
275 280 285
Lys Ser Gln Met Glu Glu Ile Ala Arg Gly Leu Leu Asp Cys Gly Arg
290 295 300
Pro Phe Leu Trp Val Val Arg Val Asn Glu Gly Glu Glu Val Leu Ile
305 310 315 320
Ser Cys Met Glu Glu Leu Lys Arg Val Gly Lys Ile Val Ser Trp Cys
325 330 335

Ser Gln Leu Glu Val Leu Thr His Pro Ser Leu Gly Cys Phe Val Thr
340 345 350

His Cys Gly Trp Asn Ser Thr Leu Glu Ser Ile Ser Phe Gly Val Pro
355 360 365

Met Val Ala Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys Leu
370 375 380

Met Glu Asp Val Trp Arg Thr Gly Val Arg Val Arg Ala Asn Glu Glu
385 390 395 400

Gly Ser Val Val Asp Gly Asp Glu Ile Arg Arg Cys Ile Glu Glu Val
405 410 415

Met Asp Gly Gly Glu Lys Ser Arg Lys Leu Arg Glu Ser Ala Gly Lys
420 425 430

Trp Lys Asp Leu Ala Arg Lys Ala Met Glu Glu Asp Gly Ser Ser Val
435 440 445

Asn Asn Leu Lys Val Phe Leu Asp Glu Val Val Gly Ile
450 455 460

<210> 7
<211> 1671
<212> DNA
<213> Torenia hybrira

<220>
<221> CDS
<222> (45)..(1478)
<220>
<221> misc_feature
<222> (64)
<223> Amino acid 64 is Xaa wherein Xaa = Cys or Phe.
<220>
<221> misc_feature
<222> (65)
<223> Amino acid 65 is Xaa wherein Xaa = Ser or Pro.

<400> 7
aacacataaa aaaaaaataa aagaagaaat aattaaataa aaaa atg gtt aac aaa 56
Met Val Asn Lys
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cgc cat att cta cta gca aca ttc cca gca caa ggc cac ata aac cct 104
Arg His Ile Leu Leu Ala Thr Phe Pro Ala Gln Gly His Ile Asn Pro 20
5 10 15

tct ctc gag ttc gcc aaa agg ctc ctc aac acc gga tac gtc gac caa 152
Ser Leu Glu Phe Ala Lys Arg Leu Leu Asn Thr Gly Tyr Val Asp Gln 35
25 30

gtc aca ttc ttc acg agt gta tac gca ttg aga cgc atg cgc ttc gaa 200
Val Thr Phe Phe Thr Ser Val Tyr Ala Leu Arg Arg Met Arg Phe Glu 50
40 45

acc gat ccg agc agc aga atc gat ttc gtg gca tkt yca gat tct tac 248
Thr Asp Pro Ser Ser Arg Ile Asp Phe Val Ala Xaa Xaa Asp Ser Tyr

55	60	65	
gat gat ggc tta aag aaa ggc gac gat ggc aaa aac tac atg tcg gag Asp Asp Gly Leu Lys Lys Gly Asp Asp Gly Lys Asn Tyr Met Ser Glu 70 75 80			296
atg aga aag cgc gga acg aag gcc tta aag gac act ctt att aag ctc Met Arg Lys Arg Gly Thr Lys Ala Leu Lys Asp Thr Leu Ile Lys Leu 85 90 95 100			344
aac gat gct gcg atg gga agt gaa tgt tac aat cgc gtg agc ttt gtg Asn Asp Ala Ala Met Gly Ser Glu Cys Tyr Asn Arg Val Ser Phe Val 105 110 115			392
gtg tac tct cat cta ttt tcg tgg gca gct gaa gtg gcg cgt gaa gtc Val Tyr Ser His Leu Phe Ser Trp Ala Ala Glu Val Ala Arg Glu Val 120 125 130			440
gac gtg ccg agt gcc ctt ctt tgg att gaa ccg gct acg gtt ttc gat Asp Val Pro Ser Ala Leu Leu Trp Ile Glu Pro Ala Thr Val Phe Asp 135 140 145			488
gtg tac tat ttt tac ttc aat ggg tat gcc gat gat atc gat gcg ggc Val Tyr Tyr Phe Tyr Phe Asn Gly Tyr Ala Asp Asp Ile Asp Ala Gly 150 155 160			536
tca gat caa atc caa ctg ccc aat ctt ccg cag ctc tcc aag caa gat Ser Asp Gln Ile Gln Leu Pro Asn Leu Pro Gln Leu Ser Lys Gln Asp 165 170 175 180			584
ctc ccc tct ttc cta ctc cct tcg agc ccc gcg aga ttc cga acc cta Leu Pro Ser Phe Leu Leu Pro Ser Ser Pro Ala Arg Phe Arg Thr Leu 185 190 195			632
atg aaa gaa aag ttc gac acg ctc gac aaa gaa ccg aaa gcg aag gtc Met Lys Glu Lys Phe Asp Thr Leu Asp Lys Glu Pro Lys Ala Lys Val 200 205 210			680
ttg ata aac acg ttc gac gca tta gaa acc gaa caa ctc aaa gcc atc Leu Ile Asn Thr Phe Asp Ala Leu Glu Thr Glu Gln Leu Lys Ala Ile 215 220 225			728
gac agg tat gaa cta ata tcc atc ggc cca tta atc cca tca tcg ata Asp Arg Tyr Glu Leu Ile Ser Ile Gly Pro Leu Ile Pro Ser Ser Ile 230 235 240			776
ttc tca gat ggc aac gac ccc tca tca agc aac aaa tcc tac ggt gga Phe Ser Asp Gly Asn Asp Pro Ser Ser Ser Asn Lys Ser Tyr Gly Gly 245 250 255 260			824
gac ctc ttc aga aaa gcc gat gaa act tac atg gac tgg cta aac tca Asp Leu Phe Arg Lys Ala Asp Glu Thr Tyr Met Asp Trp Leu Asn Ser 265 270 275			872
aaa ccc gaa tca tcg gtc gtt tac gtt tcg ttc ggg agc ctc ctg agg Lys Pro Glu Ser Ser Val Val Tyr Val Ser Phe Gly Ser Leu Leu Arg 280 285 290			920
ctc ccg aaa ccc caa atg gaa gaa ata gca ata ggg ctt tca gac acc Leu Pro Lys Pro Gln Met Glu Glu Ile Ala Ile Gly Leu Ser Asp Thr 295 300 305			968
aaa tcg cca gtt ctc tgg gtg ata aga aga aac gaa gag ggc gac gaa			1016

Lys	Ser	Pro	Val	Leu	Trp	Val	Ile	Arg	Arg	Asn	Glu	Glu	Gly	Asp	Glu		
	310					315					320						
caa	gag	caa	gca	gaa	gaa	gaa	gag	aag	ctg	ctg	agc	ttc	ttt	gat	cgt	1064	
Gln	Glu	Gln	Ala	Glu	Glu	Glu	Glu	Lys	Leu	Leu	Ser	Phe	Phe	Asp	Arg		
325					330				335					340			
cac	gga	act	gaa	cga	ctc	ggg	aaa	atc	gtg	aca	tgg	tgc	tca	caa	ttg	1112	
His	Gly	Thr	Glu	Arg	Leu	Gly	Lys	Ile	Val	Thr	Trp	Cys	Ser	Gln	Leu		
			345						350					355			
gat	gtt	ctg	acg	cat	aag	tcg	gtg	gga	tgc	ttc	gtg	acg	cat	tgc	ggg	1160	
Asp	Val	Leu	Thr	His	Lys	Ser	Val	Gly	Cys	Phe	Val	Thr	His	Cys	Gly		
			360					365					370				
tgg	aat	tct	gct	atc	gag	agc	ctg	gct	tgt	ggg	gtg	ccc	gtg	gtg	tgc	1208	
Trp	Asn	Ser	Ala	Ile	Glu	Ser	Leu	Ala	Cys	Gly	Val	Pro	Val	Val	Cys		
	375						380					385					
ttt	cct	caa	tgg	ttc	gat	caa	ggg	act	aat	gcg	aag	atg	atc	gaa	gat	1256	
Phe	Pro	Gln	Trp	Phe	Asp	Gln	Gly	Thr	Asn	Ala	Lys	Met	Ile	Glu	Asp		
	390					395					400						
gtg	tgg	agg	agt	ggg	gtg	aga	gtc	aga	gtg	aat	gag	gaa	ggc	ggc	gtt	1304	
Val	Trp	Arg	Ser	Gly	Val	Arg	Val	Arg	Val	Asn	Glu	Glu	Gly	Gly	Val		
405					410				415						420		
gtt	gat	agg	cgt	gag	att	aag	agg	tgc	gtc	tcg	gag	gtt	ata	aag	agt	1352	
Val	Asp	Arg	Arg	Glu	Ile	Lys	Arg	Cys	Val	Ser	Glu	Val	Ile	Lys	Ser		
				425					430					435			
cga	gag	ttg	aga	gaa	agc	gca	atg	atg	tgg	aag	ggg	ttg	gct	aaa	gaa	1400	
Arg	Glu	Leu	Arg	Glu	Ser	Ala	Met	Met	Trp	Lys	Gly	Leu	Ala	Lys	Glu		
			440					445					450				
gct	atg	gat	gaa	gaa	cgt	gga	tca	tca	atg	aac	aat	ctg	aag	aat	ttt	1448	
Ala	Met	Asp	Glu	Glu	Arg	Gly	Ser	Ser	Met	Asn	Asn	Leu	Lys	Asn	Phe		
		455					460					465					
att	act	agg	att	att	aat	gaa	aat	gcc	tca	taagttgtac	tatatatgtt					1498	
Ile	Thr	Arg	Ile	Ile	Asn	Glu	Asn	Ala	Ser								
	470					475											
attattgttg	ttatggacgt	cgaattaagt	attagttaaa	tgatatgtat	ttagaggaag											1558	
gccaaaacgg	gctacacccg	gcaggccacg	ggttggaaaa	gcccgccatg	atttaaaata											1618	
tatatatttaa	aataaatatt	ttctactatt	aaactaaaaa	aaaaaaaaaa	aaa											1671	

<210> 8
 <211> 478
 <212> PRT
 <213> Torenia hybrira

<400> 8
 Met Val Asn Lys Arg His Ile Leu Leu Ala Thr Phe Pro Ala Gln Gly
 1 5 10 15
 His Ile Asn Pro Ser Leu Glu Phe Ala Lys Arg Leu Leu Asn Thr Gly
 20 25 30
 Tyr Val Asp Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Leu Arg Arg

35					40					45					
Met	Arg	Phe	Glu	Thr	Asp	Pro	Ser	Ser	Arg	Ile	Asp	Phe	Val	Ala	Xaa
	50					55					60				
Xaa	Asp	Ser	Tyr	Asp	Asp	Gly	Leu	Lys	Lys	Gly	Asp	Asp	Gly	Lys	Asn
65				70						75					80
Tyr	Met	Ser	Glu	Met	Arg	Lys	Arg	Gly	Thr	Lys	Ala	Leu	Lys	Asp	Thr
				85					90					95	
Leu	Ile	Lys	Leu	Asn	Asp	Ala	Ala	Met	Gly	Ser	Glu	Cys	Tyr	Asn	Arg
			100					105					110		
Val	Ser	Phe	Val	Val	Tyr	Ser	His	Leu	Phe	Ser	Trp	Ala	Ala	Glu	Val
		115					120					125			
Ala	Arg	Glu	Val	Asp	Val	Pro	Ser	Ala	Leu	Leu	Trp	Ile	Glu	Pro	Ala
	130					135					140				
Thr	Val	Phe	Asp	Val	Tyr	Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ala	Asp	Asp
145				150						155					160
Ile	Asp	Ala	Gly	Ser	Asp	Gln	Ile	Gln	Leu	Pro	Asn	Leu	Pro	Gln	Leu
				165					170					175	
Ser	Lys	Gln	Asp	Leu	Pro	Ser	Phe	Leu	Leu	Pro	Ser	Ser	Pro	Ala	Arg
			180					185					190		
Phe	Arg	Thr	Leu	Met	Lys	Glu	Lys	Phe	Asp	Thr	Leu	Asp	Lys	Glu	Pro
		195					200					205			
Lys	Ala	Lys	Val	Leu	Ile	Asn	Thr	Phe	Asp	Ala	Leu	Glu	Thr	Glu	Gln
	210					215					220				
Leu	Lys	Ala	Ile	Asp	Arg	Tyr	Glu	Leu	Ile	Ser	Ile	Gly	Pro	Leu	Ile
225				230						235					240
Pro	Ser	Ser	Ile	Phe	Ser	Asp	Gly	Asn	Asp	Pro	Ser	Ser	Ser	Asn	Lys
				245					250					255	
Ser	Tyr	Gly	Gly	Asp	Leu	Phe	Arg	Lys	Ala	Asp	Glu	Thr	Tyr	Met	Asp
			260					265					270		
Trp	Leu	Asn	Ser	Lys	Pro	Glu	Ser	Ser	Val	Val	Tyr	Val	Ser	Phe	Gly
		275					280					285			
Ser	Leu	Leu	Arg	Leu	Pro	Lys	Pro	Gln	Met	Glu	Glu	Ile	Ala	Ile	Gly
	290					295					300				
Leu	Ser	Asp	Thr	Lys	Ser	Pro	Val	Leu	Trp	Val	Ile	Arg	Arg	Asn	Glu
305					310					315					320
Glu	Gly	Asp	Glu	Gln	Glu	Gln	Ala	Glu	Glu	Glu	Glu	Lys	Leu	Leu	Ser
				325					330					335	
Phe	Phe	Asp	Arg	His	Gly	Thr	Glu	Arg	Leu	Gly	Lys	Ile	Val	Thr	Trp
			340					345					350		
Cys	Ser	Gln	Leu	Asp	Val	Leu	Thr	His	Lys	Ser	Val	Gly	Cys	Phe	Val
		355					360					365			
Thr	His	Cys	Gly	Trp	Asn	Ser	Ala	Ile	Glu	Ser	Leu	Ala	Cys	Gly	Val

370	375	380
Pro Val Val Cys Phe 385	Pro Gln Trp Phe Asp 390	Gln Gly Thr Asn Ala Lys 395 400
Met Ile Glu Asp Val Trp Arg Ser Gly Val Arg Val Arg Val Asn Glu 405 410 415		
Glu Gly Gly Val Val Asp Arg Arg Glu Ile Lys Arg Cys Val Ser Glu 420 425 430		
Val Ile Lys Ser Arg Glu Leu Arg Glu Ser Ala Met Met Trp Lys Gly 435 440 445		
Leu Ala Lys Glu Ala Met Asp Glu Glu Arg Gly Ser Ser Met Asn Asn 450 455 460		
Leu Lys Asn Phe Ile Thr Arg Ile Ile Asn Glu Asn Ala Ser 465 470 475		

<210> 9
 <211> 1437
 <212> DNA
 <213> *Perilla frutescens*

<220>
 <221> CDS
 <222> (294)..(1298)

<400> 9
 ttcaaaactc ataacgtgat tgagctaattg tgcacatctt cctcttcaaa gtctacagtg 60
 tcctcctacc agcatcatca tgatcaatct ctttataatg aggagaatgg agtaacaagg 120
 agtggggtttt gttactcagc ttcaacctac gtacgtacta ctactgactc aactctcaag 180
 agaatgaata taatatataa tgggcgatag atctttgtag atatgtaggt gtagcctgca 240
 ggtgggtaat taatttccgg tgtgggaaaa taaataaata aataaatata gcg atg 296
 Met
 1
 agc agc agc agc agc aga agg tgg aga gag aat gag ggg atg cga agg 344
 Ser Ser Ser Ser Ser Arg Arg Trp Arg Glu Asn Glu Gly Met Arg Arg
 5 10 15
 aca ttg ctg ggg ttg ggt ttg ggg cag ttg gtt tct ttc gat ttg gct 392
 Thr Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu Ala
 20 25 30
 atc atg acc ttt tct gct tct ttg gtt tca acc aca gtg gat gca cca 440
 Ile Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala Pro
 35 40 45
 ctt act atg tcg ttc act aca tac act gtt gtg gcc ctg ctc tat gga 488
 Leu Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr Gly
 50 55 60 65
 acc atc ttg ctt tac cgc cgc cac aaa ttc ttg gtt cca tgg tac tgg 536
 Thr Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr Trp
 70 75 80

tat gct ctc ctg ggg ttc gtg gac gtc cac ggc aat tat ctt gtt aat	584
Tyr Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val Asn	
85 90 95	
aaa gca ttc gag ttg aca tcg att acg agt gtg agc ata ctg gat tgt	632
Lys Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp Cys	
100 105 110	
tgg aca atc gtg tgg tcc atc atc ttt aca tgg atg ttc cta ggc aca	680
Trp Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly Thr	
115 120 125	
aaa tac tct gta tac cag ttt gtc ggt gct gct att tgt gta gga ggc	728
Lys Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly Gly	
130 135 140 145	
ctc ctc ctc gtg ctt ctt tcc gac tca ggg gtc act gct gct ggt tcg	776
Leu Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly Ser	
150 155 160	
aat cct ctt ttg ggt gat ttt ctt gtc ata aca ggc tct att ttg ttc	824
Asn Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu Phe	
165 170 175	
aca ctc agc act gtt ggt cag gaa tac tgc gtg aag agg aaa gat cgt	872
Thr Leu Ser Thr Val Gly Gln Tyr Cys Val Lys Arg Lys Asp Arg	
180 185 190	
att gaa gta gta gca atg atc ggt gta ttt ggt atg ctc atc agt gca	920
Ile Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser Ala	
195 200 205	
acc gag att act gtg ctg gag agg aat gcc ctc tca tca atg cag tgg	968
Thr Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln Trp	
210 215 220 225	
tct act gga ctt ttg gca gcc tat gtt gtt tat gca ctg tcc agc ttc	1016
Ser Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser Phe	
230 235 240	
ctc ttc tgc aca ctc acc cct ttt ctt ctc aag atg agt ggc gct gca	1064
Leu Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala Ala	
245 250 255	
ttt ttc aat ctt tcc atg ctt aca tct gat atg tgg gct gtt gca att	1112
Phe Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala Ile	
260 265 270	
agg aca ttc ata tac aac cag gag gtt gat tgg tta tac tat ttg gcc	1160
Arg Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu Ala	
275 280 285	
ttt tgt ctc gtt gtt gtt gga ata ttc ata tat aca aaa aca gag aag	1208
Phe Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu Lys	
290 295 300 305	
gat cct aac aat acg aga gcc ctt gag aat gga aac ttg gat cat gaa	1256
Asp Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His Glu	
310 315 320	
tat agt ctc ctt gag gat caa gat gac aca cca aga aaa cca	1298
Tyr Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro	
325 330 335	

tagctagctt tgccacaat cttttcatca acagttttta ataatcgtg aggggggagag 1358
 agatcgagat actaattaat ggacgtctat tatatagttg gaggtttttg ttttatttat 1418
 ttatttgagt aaaaaaaaaa 1437

<210> 10
 <211> 335
 <212> PRT
 <213> *Perilla frutescens*

<400> 10
 Met Ser Ser Ser Ser Ser Arg Arg Trp Arg Glu Asn Glu Gly Met Arg
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 Arg Thr Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu
 20 25 30
 Ala Ile Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala
 35 40 45
 Pro Leu Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr
 50 55 60
 Gly Thr Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr
 65 70 75 80
 Trp Tyr Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val
 85 90 95
 Asn Lys Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp
 100 105 110
 Cys Trp Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly
 115 120 125
 Thr Lys Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly
 130 135 140
 Gly Leu Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly
 145 150 155 160
 Ser Asn Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu
 165 170 175
 Phe Thr Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp
 180 185 190
 Arg Ile Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser
 195 200 205
 Ala Thr Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln
 210 215 220
 Trp Ser Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser
 225 230 235 240
 Phe Leu Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala
 245 250 255
 Ala Phe Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala
 260 265 270

Ile Arg Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu
275 280 285

Ala Phe Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu
290 295 300

Lys Asp Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His
305 310 315 320

Glu Tyr Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro
325 330 335

<210> 11
<211> 2105
<212> DNA
<213> Petunia hybrida

<220>
<221> CDS
<222> (341)..(1744)

<400> 11
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tttatgcttc cggctcgtat gttgtgtgga attgtgagcg gataacaatt tcacacagga 120
aacagctatg accatgatta cgccaagctc gaaattaacc ctcactaaag ggaacaaaag 180
ctggagctcc acgcggtggc ggccgctcta gaactagtgg atcccccgga ctgcaggaat 240
tccgttgctg tcgccacaat ttacaaacca agaaattaag catccctttc ccccccttaa 300
aaaacataca agtttttaat ttttcactaa gcaagaaaat atg gtg cag cct cat 355
Met Val Gln Pro His
1 5

gtc atc tta aca aca ttt cca gca caa ggc cat att aat cca gca ctt 403
Val Ile Leu Thr Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu
10 15 20

caa ttt gcc aag aat ctt gtc aag atg ggc ata gaa gtg aca ttt tct 451
Gln Phe Ala Lys Asn Leu Val Lys Met Gly Ile Glu Val Thr Phe Ser
25 30 35

aca agc att tat gcc caa agc cgt atg gat gaa aaa tcc att ctt aat 499
Thr Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu Lys Ser Ile Leu Asn
40 45 50

gca cca aaa gga ttg aat ttc att cca ttt tcc gat ggc ttt gat gaa 547
Ala Pro Lys Gly Leu Asn Phe Ile Pro Phe Ser Asp Gly Phe Asp Glu
55 60 65

ggc ttt gat cat tca aaa gac cct gta ttt tac atg tca caa ctt cgt 595
Gly Phe Asp His Ser Lys Asp Pro Val Phe Tyr Met Ser Gln Leu Arg
70 75 80 85

aaa tgt gga agt gaa act gtc aaa aaa ata att ctc act tgc tct gaa 643
Lys Cys Gly Ser Glu Thr Val Lys Lys Ile Ile Leu Thr Cys Ser Glu
90 95 100

aat gga cag cct ata act tgc cta ctt tac tcc att ttc ctt cct tgg 691
Asn Gly Gln Pro Ile Thr Cys Leu Leu Tyr Ser Ile Phe Leu Pro Trp

105										110					115					
gca	gca	gag	gta	gca	cgt	gaa	gtt	cac	atc	cct	tct	gct	ctt	ctt	tgg	739				
Ala	Ala	Glu	Val	Ala	Arg	Glu	Val	His	Ile	Pro	Ser	Ala	Leu	Leu	Trp					
		120					125					130								
agt	caa	cca	gca	aca	ata	ttg	gac	ata	tat	tac	ttc	aac	ttt	cat	gga	787				
Ser	Gln	Pro	Ala	Thr	Ile	Leu	Asp	Ile	Tyr	Tyr	Phe	Asn	Phe	His	Gly					
	135					140					145									
tat	gaa	aaa	gct	atg	gct	aat	gaa	tcc	aat	gat	cca	aat	tgg	tcc	att	835				
Tyr	Glu	Lys	Ala	Met	Ala	Asn	Glu	Ser	Asn	Asp	Pro	Asn	Trp	Ser	Ile					
150					155					160					165					
caa	ctt	ccc	ggg	ctt	cca	cta	ctg	gaa	act	cga	gat	ctt	cct	tca	ttt	883				
Gln	Leu	Pro	Gly	Leu	Pro	Leu	Leu	Glu	Thr	Arg	Asp	Leu	Pro	Ser	Phe					
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 Leu Thr Cys Ser Glu Asn Gly Gln Pro Ile Thr Cys Leu Leu Tyr Ser
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 Ser Ala Leu Leu Trp Ser Gln Pro Ala Thr Ile Leu Asp Ile Tyr Tyr
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 405 410 415

Arg Cys Ile Glu Leu Val Met Asp Gly Gly Glu Lys Gly Glu Glu Leu
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Arg Lys Asn Ala Lys Lys Trp Lys Glu Leu Ala Arg Glu Ala Val Lys
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Glu Gly Gly Ser Ser His Lys Asn Leu Lys Ala Phe Ile Asp Asp Val
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